

PhD progress update

Science Girls, cholera, chimps, and ref genomes

Emilie Jensen

Overview

- Science Girls
- Project #2: Update on Frontline metagenomics manuscript
- Project #3: Gut microbiome of Tanzanian chimpanzees
- Project #4: Genome reference project

Science girls



**LYNGBY-
TAARBÆK
AVIS**

Lokale nyheder fra
Lyngby-Taarbæk & omegn

SPORT BØRN & UNGE DEBAT & POLITIK ERH



DNA-detektiver for en aften

HANS-JØRGEN BUNDGAARD 13. MAJ 2020 ALLE NYHEDER



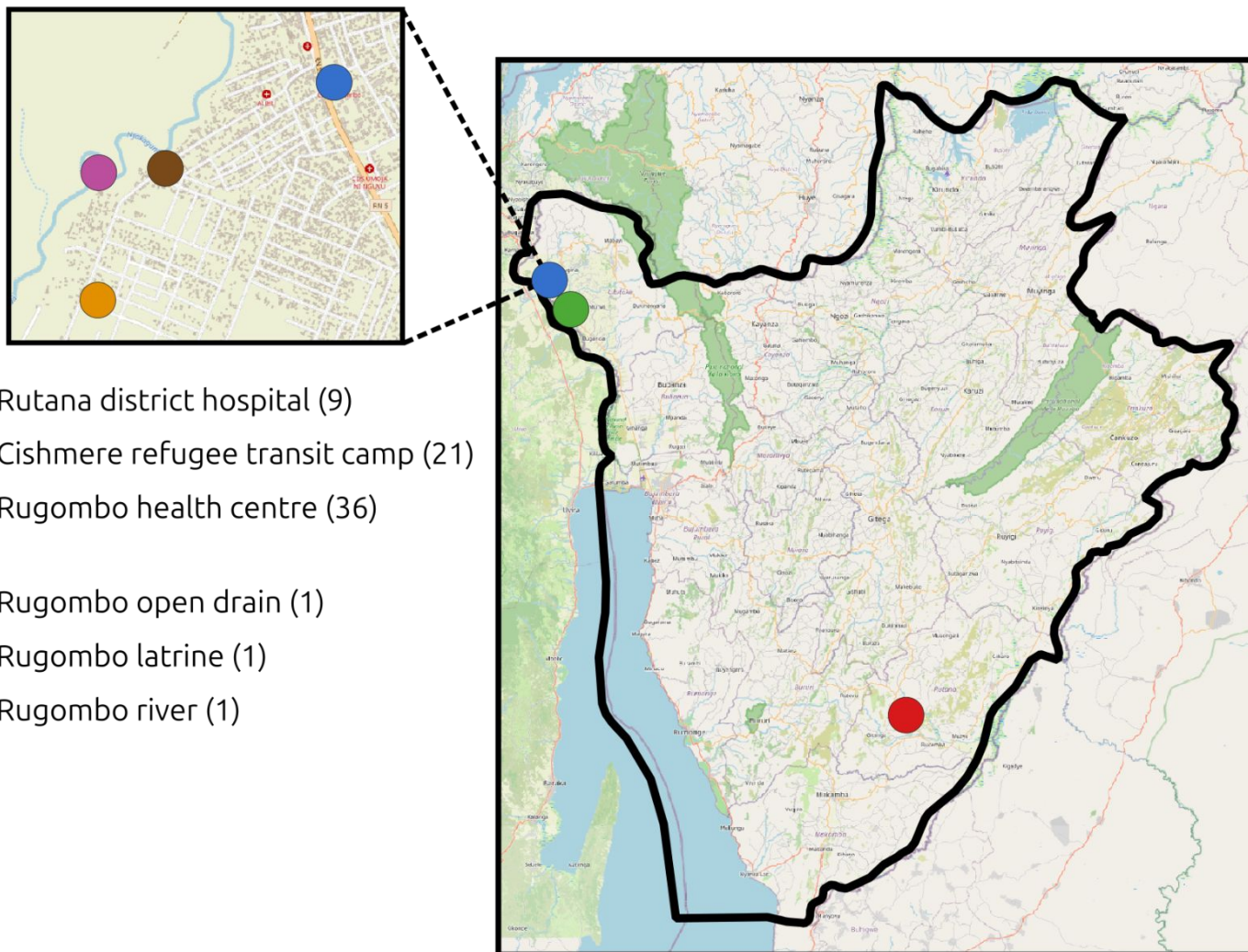
Project #2

Frontline diagnostics with metagenomics



Frontline diagnostics with metagenomics





RESEARCH ARTICLE

Syndromic cholera diagnosis masks diverse causes of diarrhoeal disease in Burundi revealed by portable metagenomics

Emilie Egholm Bruun Jensen^{1†}, Néhémie Nzoyikorera^{2†}, Mirena Ivanova¹, Pimlapas Leekitcharoenphon¹, Marie Noelle Uwineza², Idrissa Diawara^{3,4,5}, Joseph Nyandwi^{6,7}, Frank M. Aarestrup¹, Saria Otani^{1*}

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† EEBJ and NN share co-authorship on this work.

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OPEN ACCESS

Citation: Egholm Bruun Jensen E, Nzoyikorera N, Ivanova M, Leekitcharoenphon P, Noelle Uwineza M, Diawara I, et al. (2026) Syndromic cholera diagnosis masks diverse causes of diarrhoeal disease in Burundi revealed by portable metagenomics. PLoS Negl Trop Dis

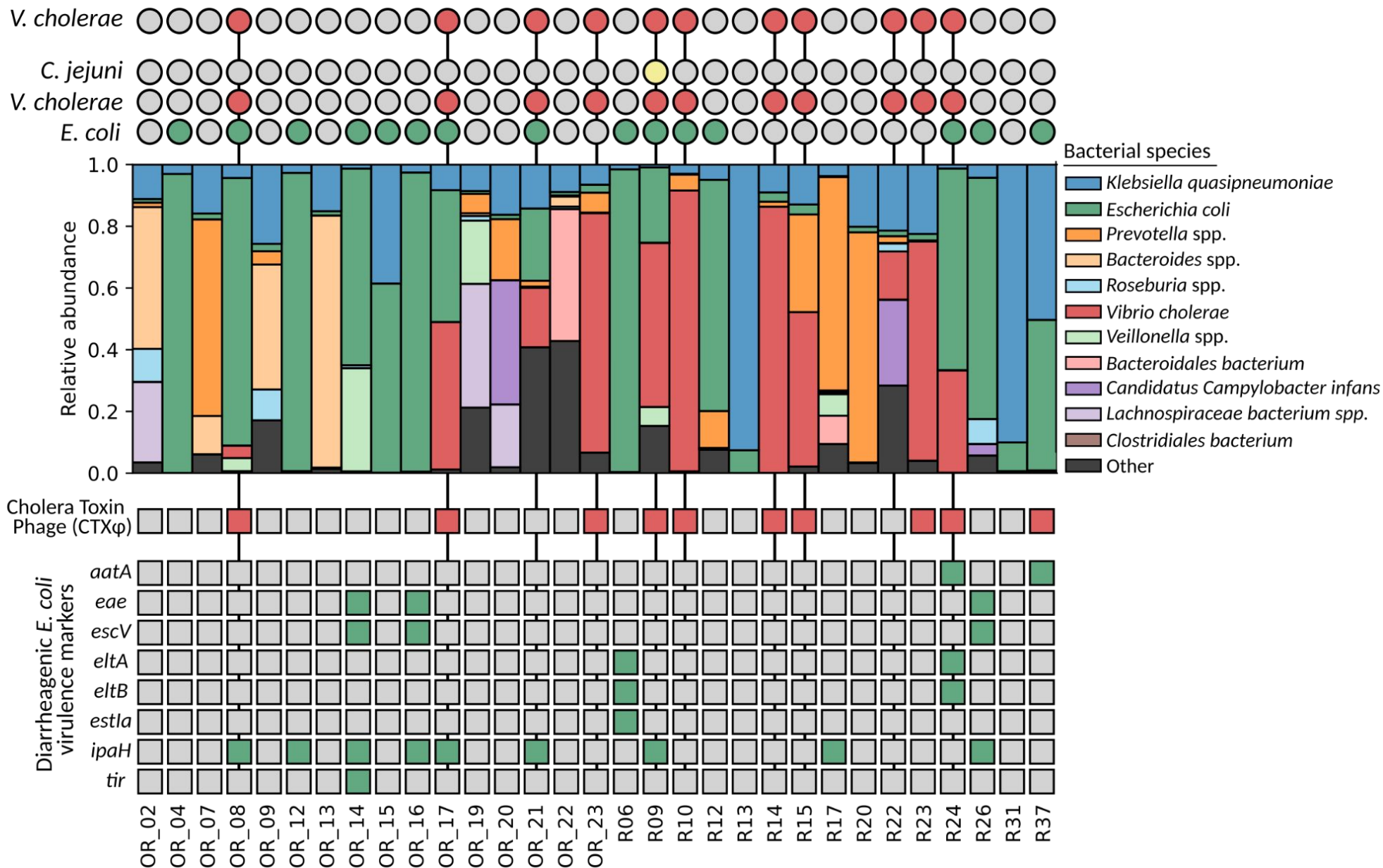
Abstract

Background

Cholera outbreaks remain a major public-health challenge in sub-Saharan Africa, where diagnostic capacity is limited and clinical case definitions are non-specific and

Frontline Culturing

HPC-based analysis



Project #3

Seasonal adaptation within the gut microbiome of wild Tanzanian chimpanzees

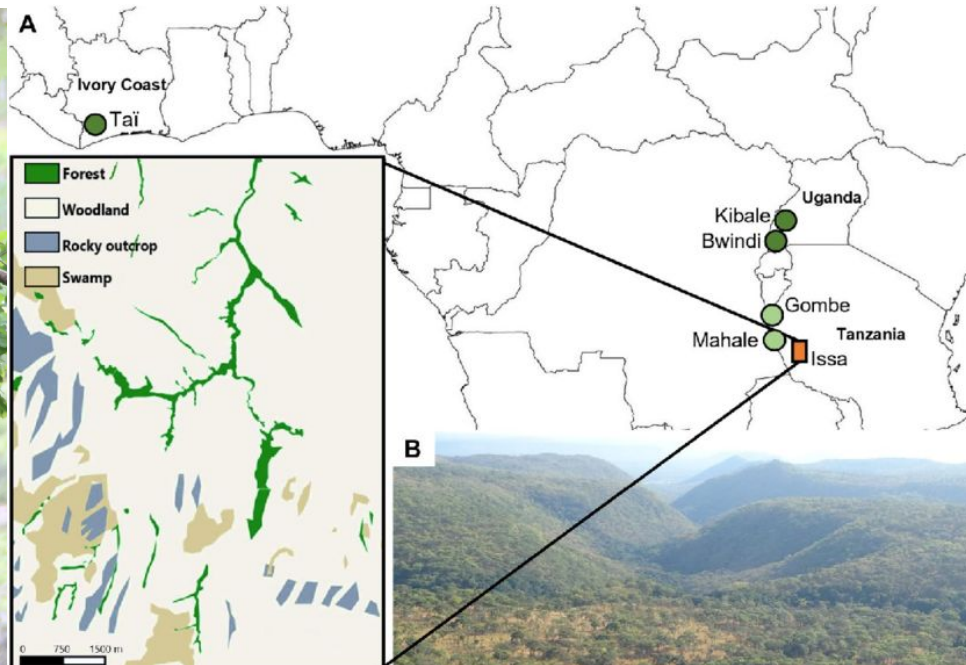


Alexander Piel and Fiona Steward
Evolutionary Anthropology
University College London

Greater Mahale Ecosystem Research and Conservation

*"We strive to **understand**, **conserve**, and **protect** primates and their behavioural diversity in the Greater Mahale Ecosystem in Western Tanzania."*

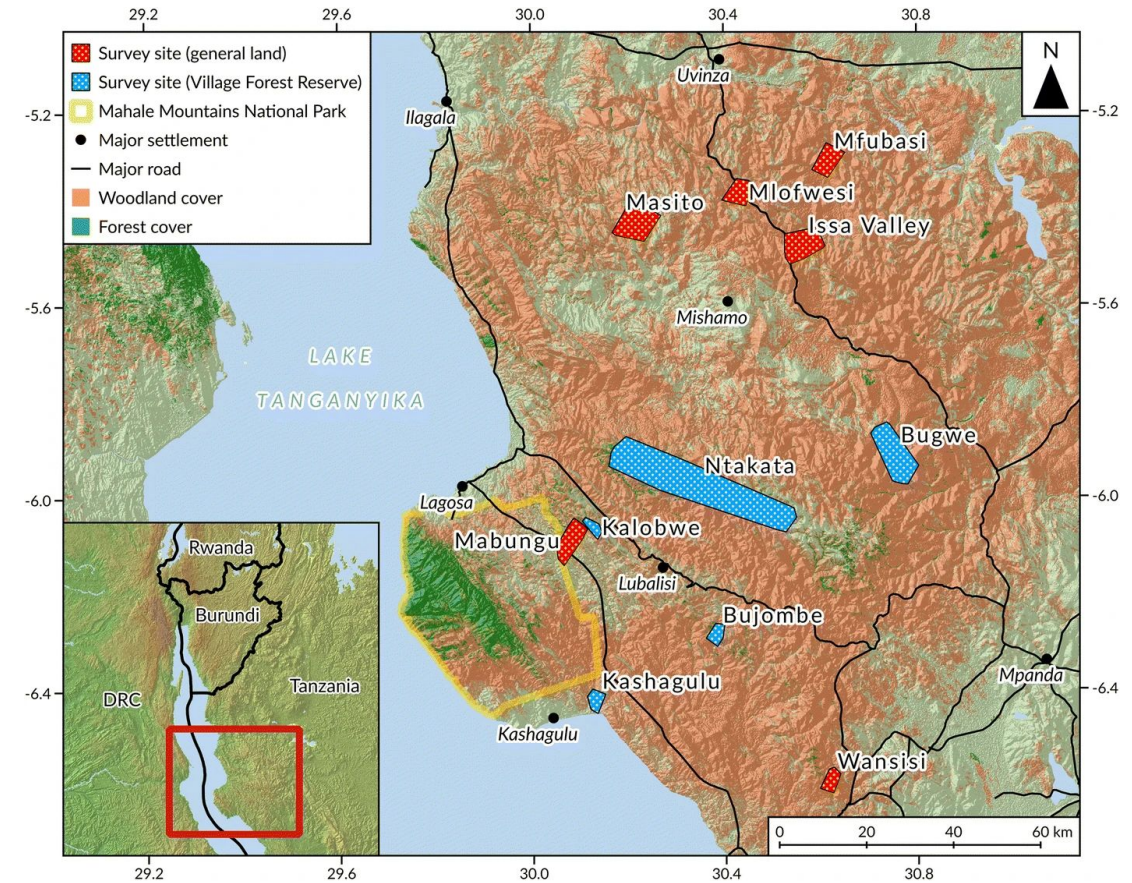
<https://www.gmerc.org/>



Mosaic landscape

Diverse and **patchy** environment with multiple habitat types:

- Miombo woodlands
- Gallery forests
- Swamps and wetland
- Wooded grasslands



McLester et al. 2019: <https://doi.org/10.1007/s10764-019-00118-6>

Seasonal variation

Wet season

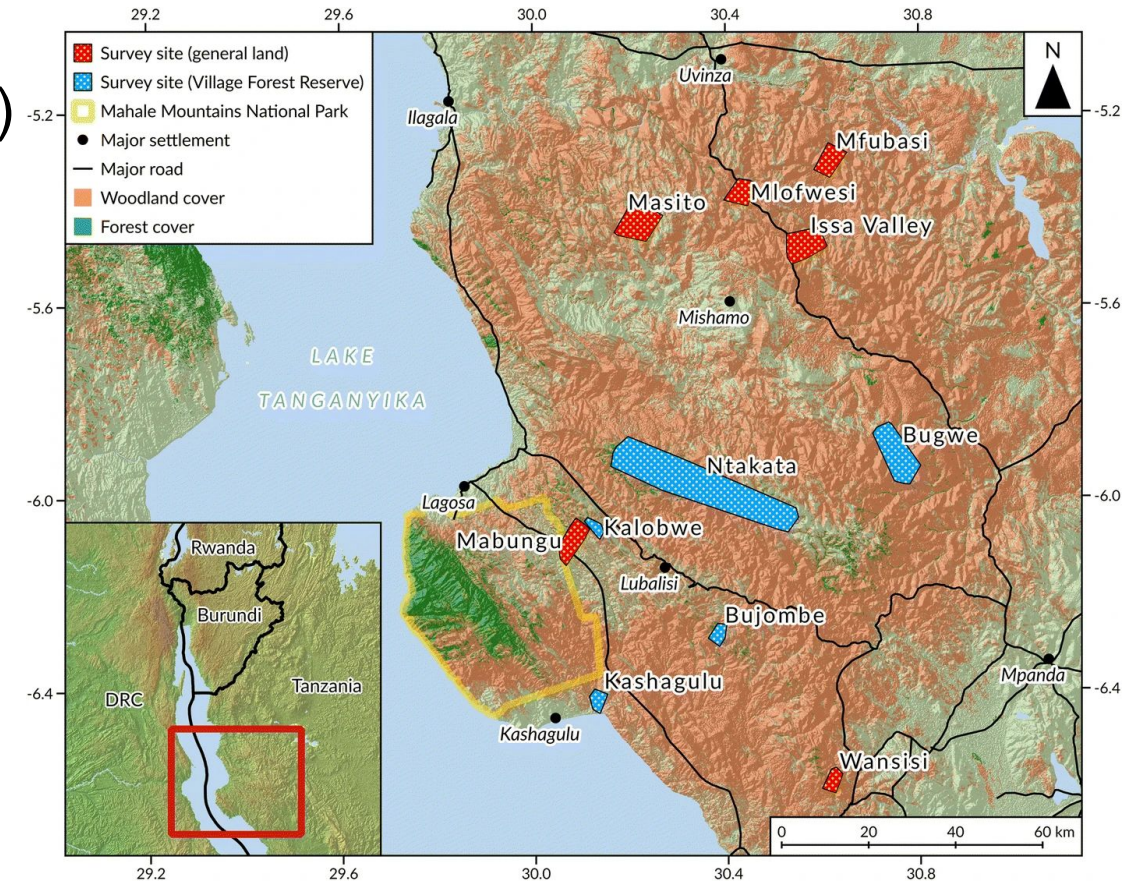
- High annual rainfall (up to 700 mm/year)
- Grass reach 2.5 m

Dry season

- Scarcity of surface water in dry season
- Grass fire depleting 75% of the region



@GMERC



McLester et al. 2019: <https://doi.org/10.1007/s10764-019-00118-6>

Does the functional gut microbiome adapt to the season changes?



Samples



557 fecal samples
from Greater Mahale
Ecosystem

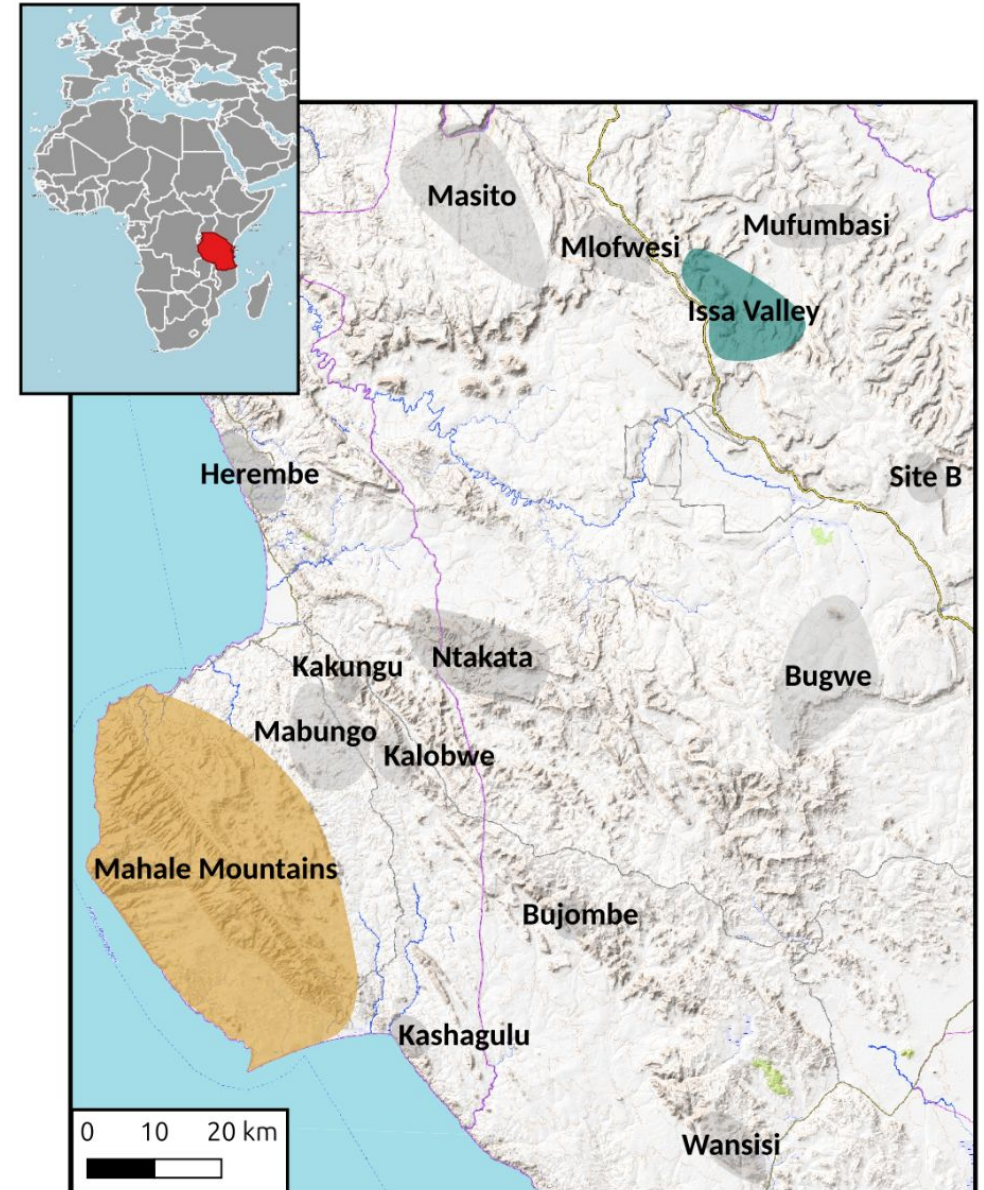


Samples were collected
from 2009 - 2020



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University College London

A



Samples



557 fecal samples
from Greater Mahale
Ecosystem

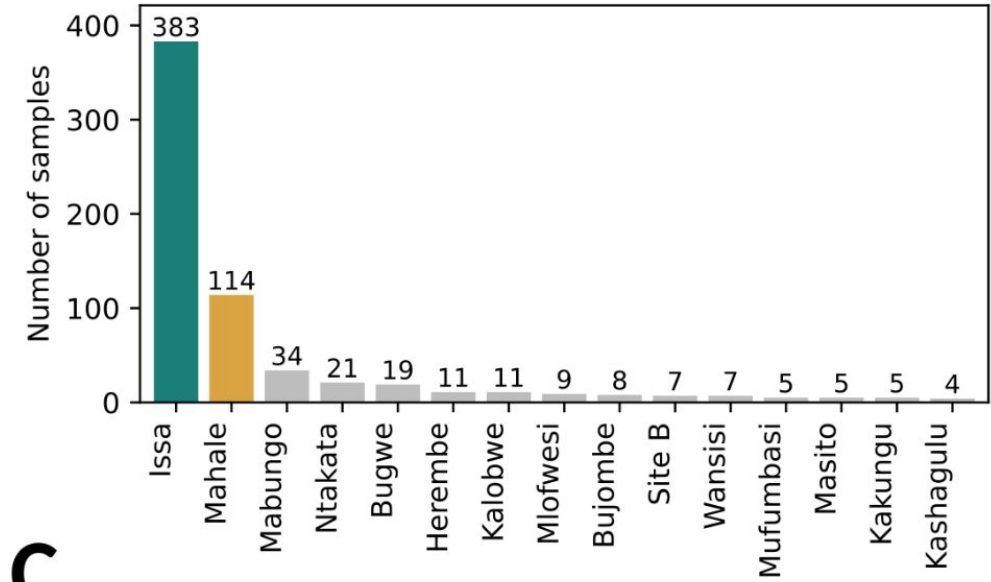


Samples were collected
from 2009 - 2020

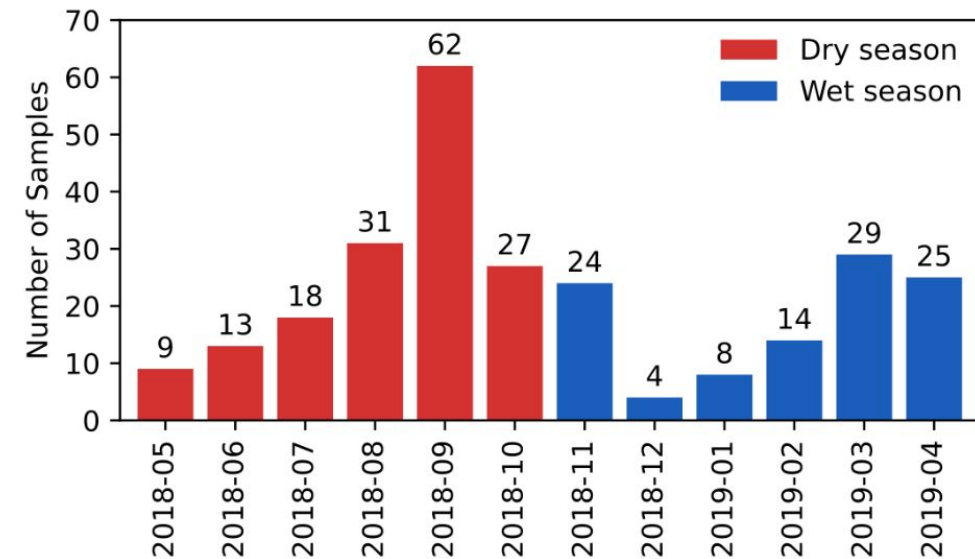


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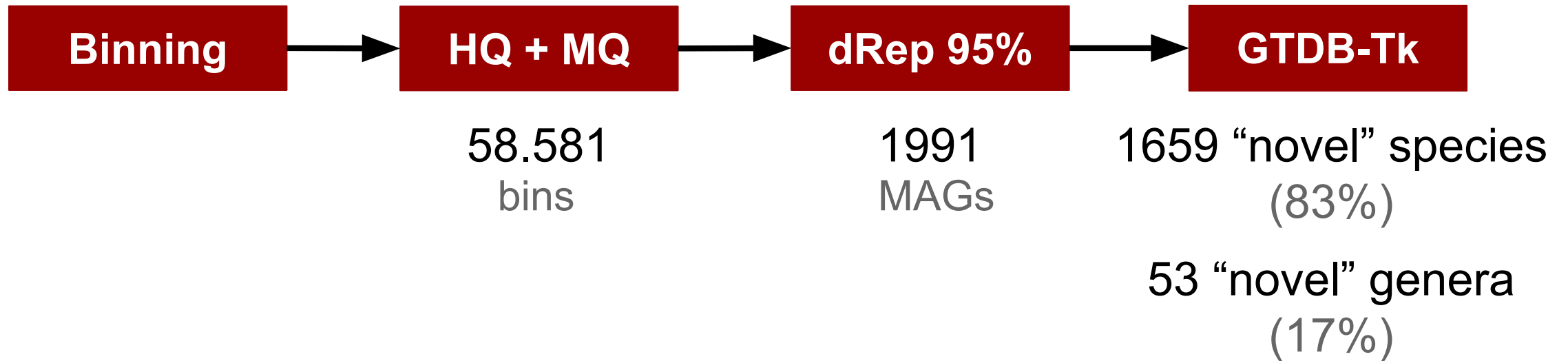
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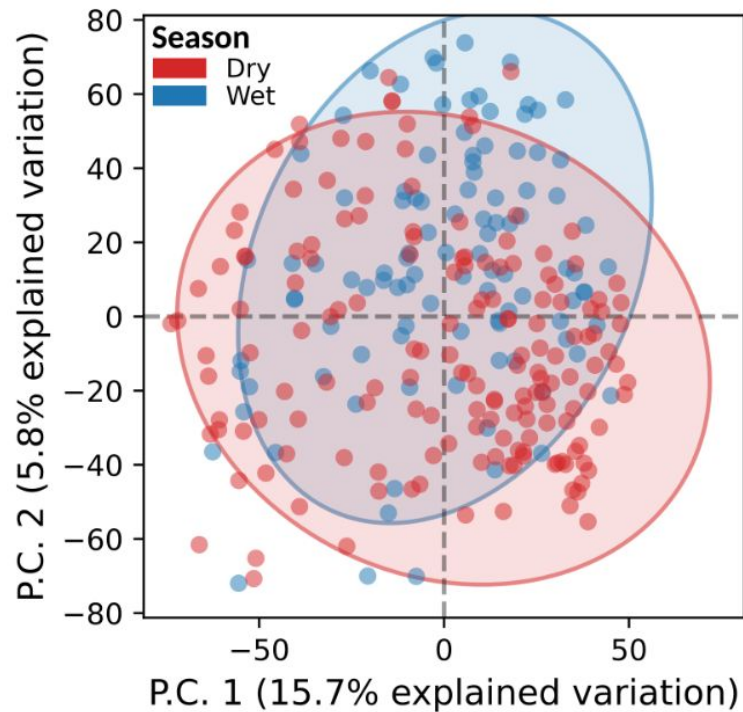
C



MAG catalogue and novel taxa

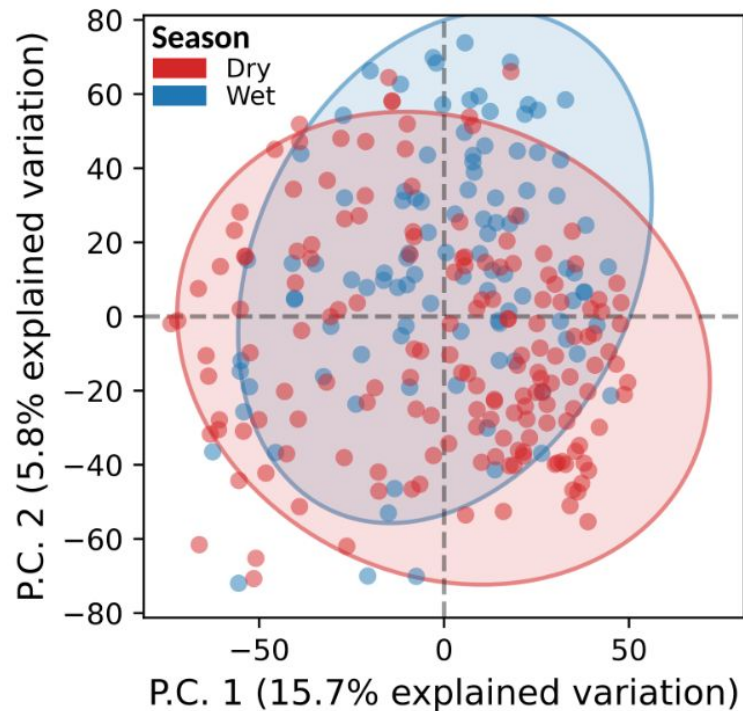


Seasonal differences: Bacterial taxa

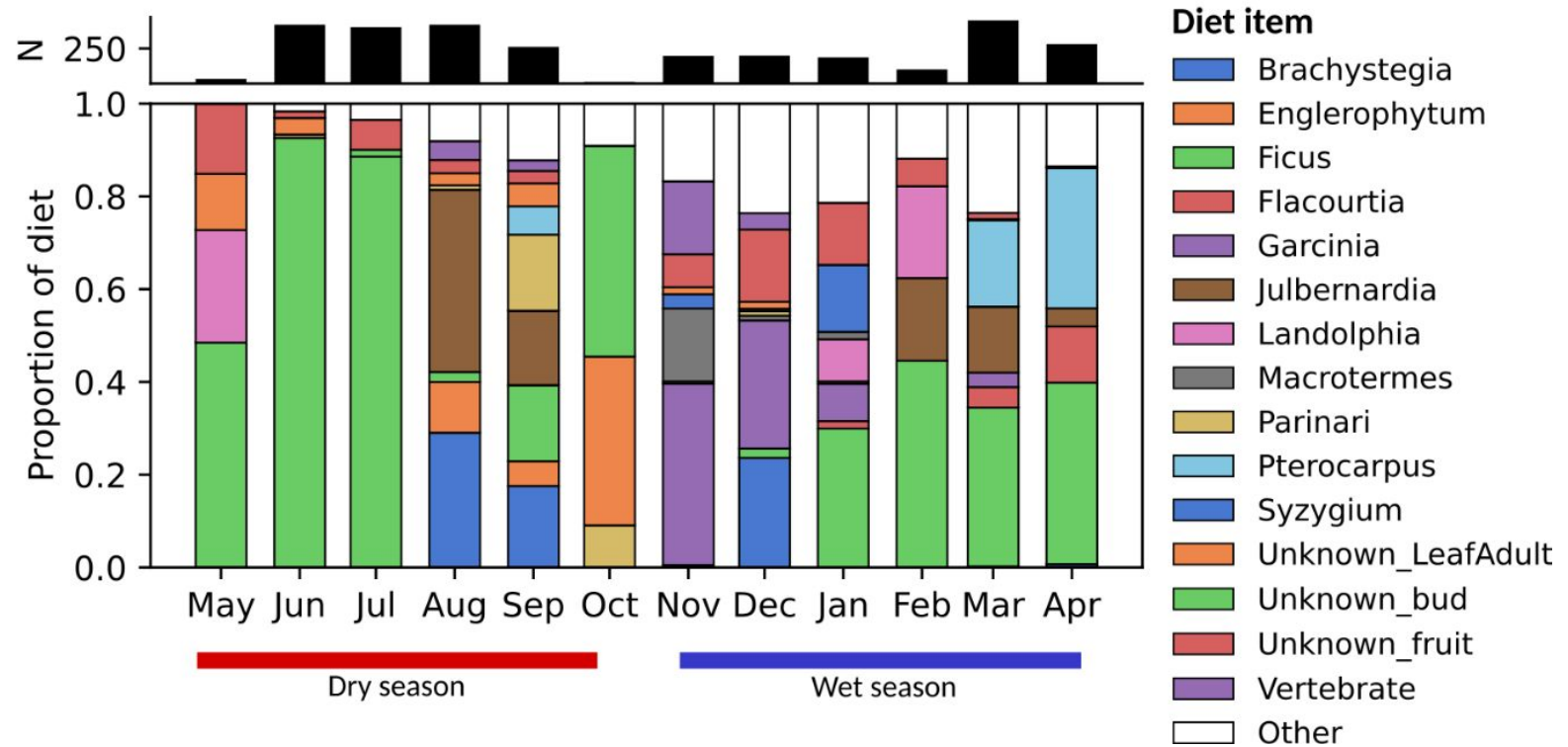
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Seasonal differences: Bacterial taxa

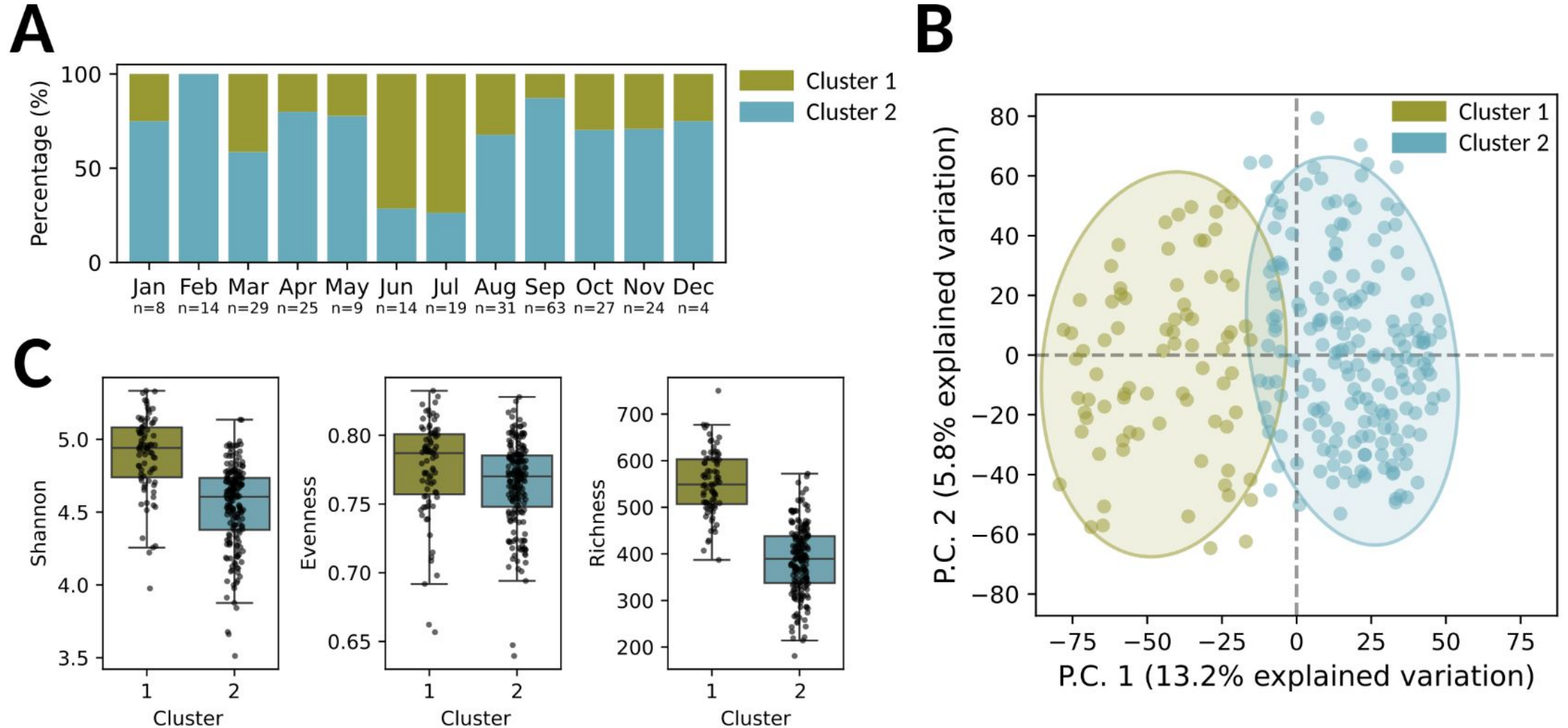
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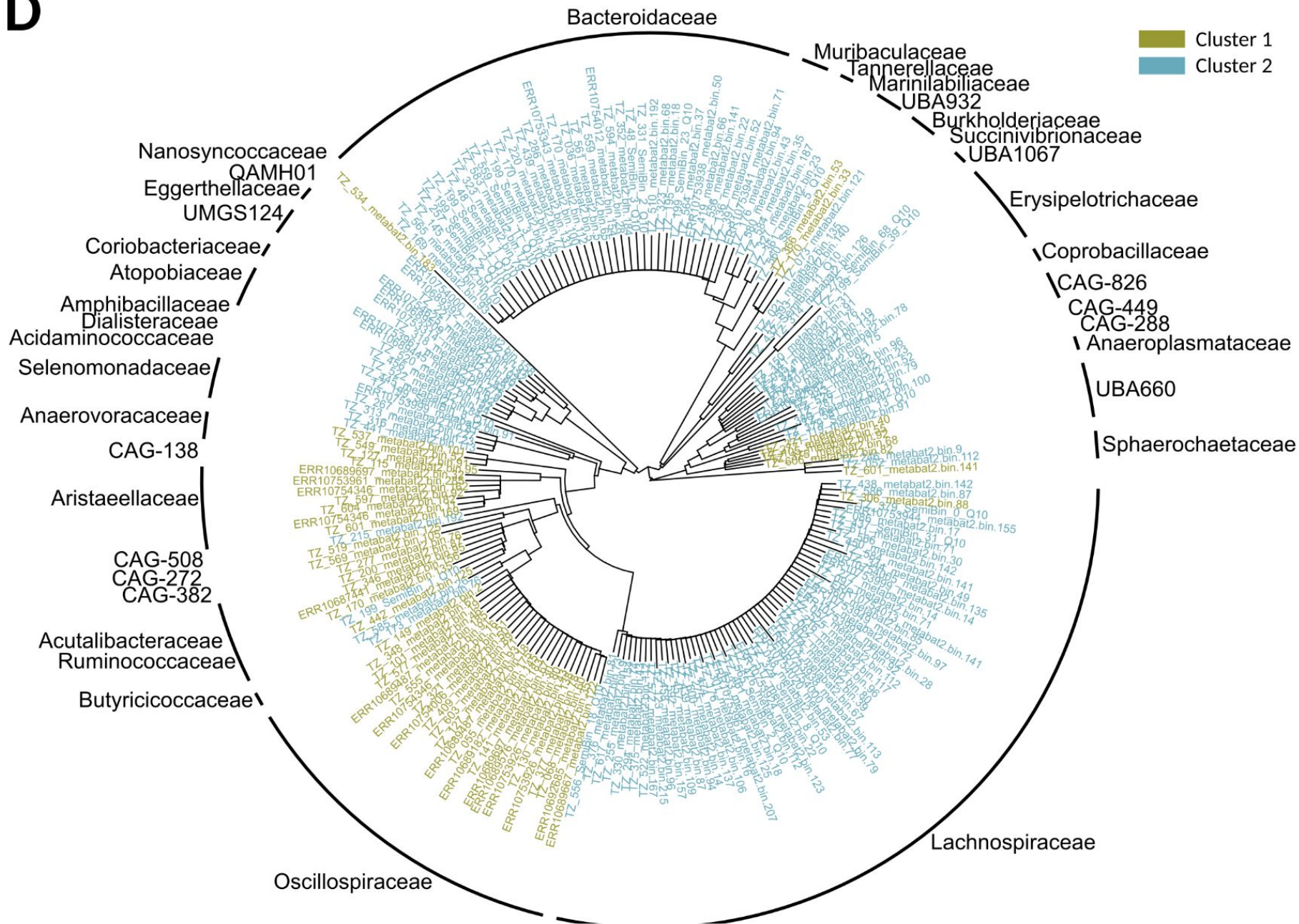


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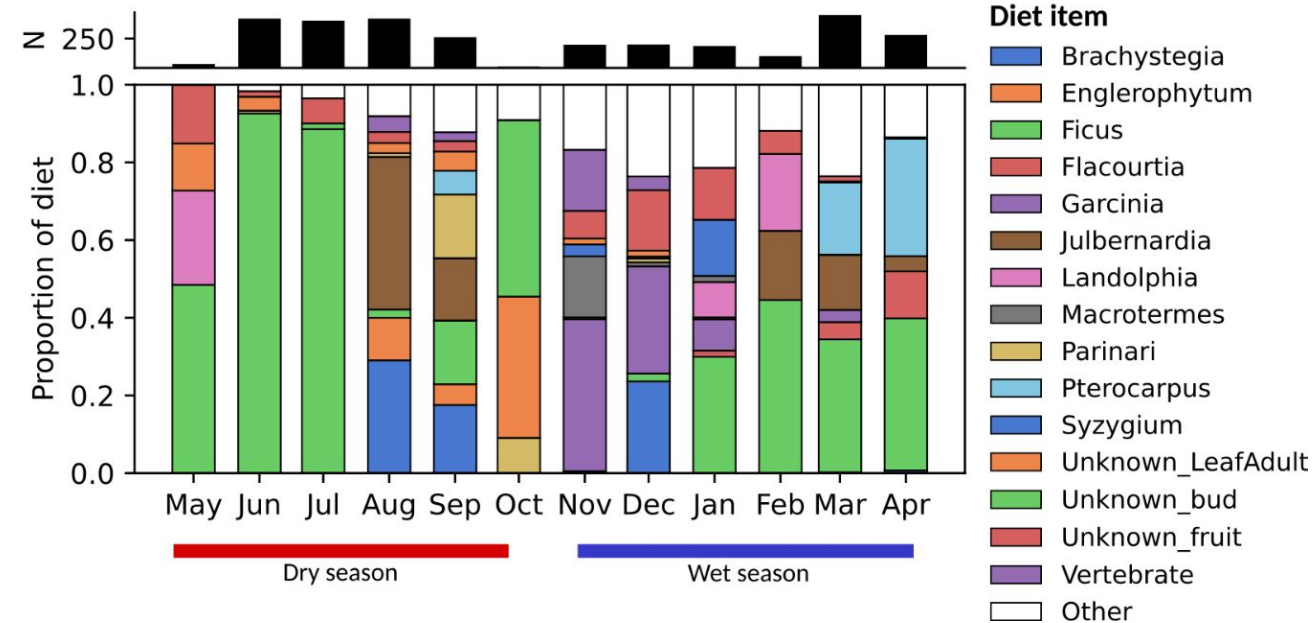
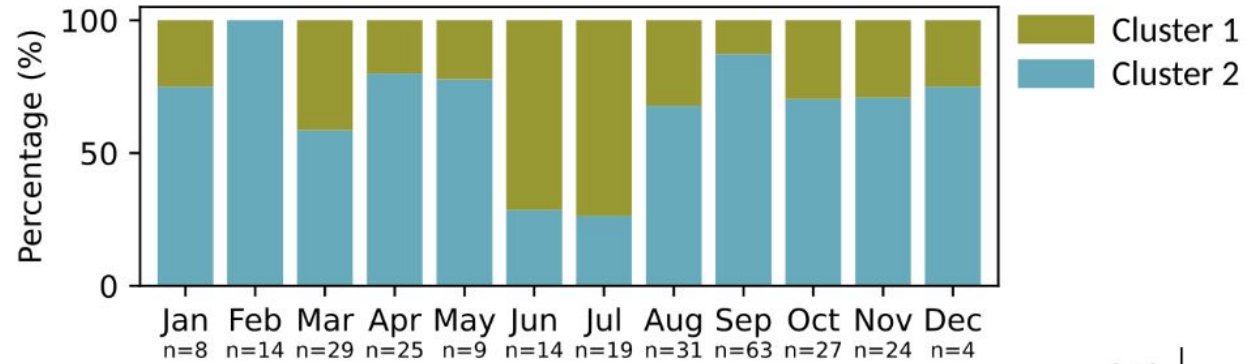
Seasonal differences: Bacterial taxa





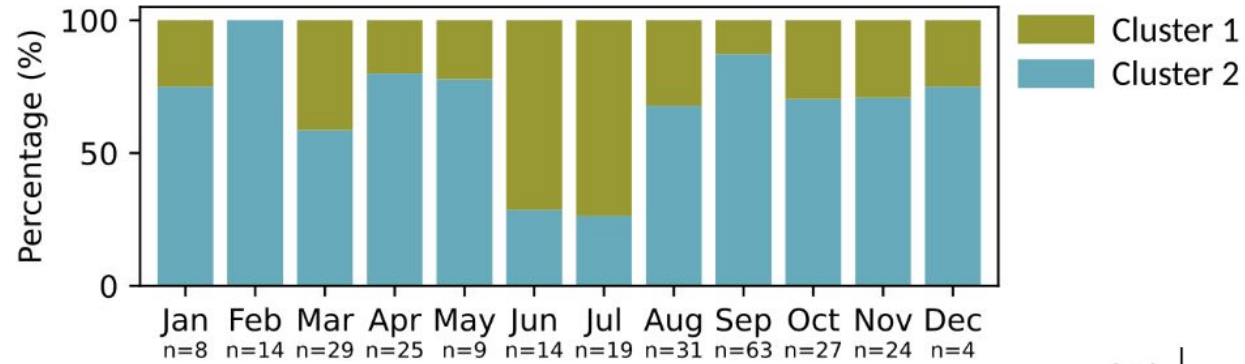
Seasonal differences: Bacterial taxa

A

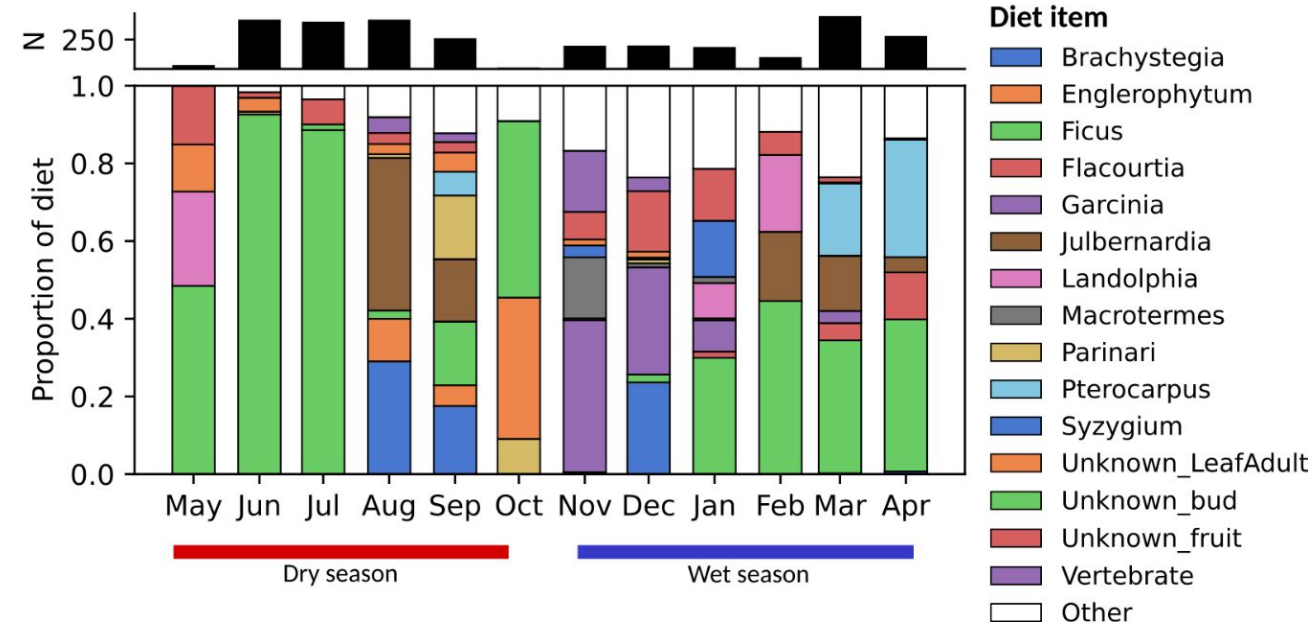


Seasonal differences: Bacterial taxa

A

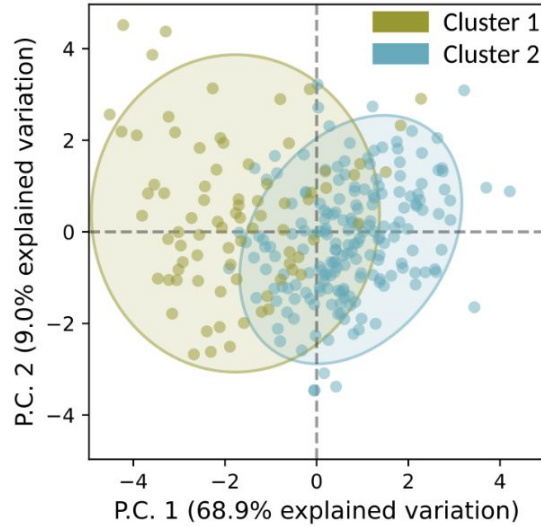


Why?

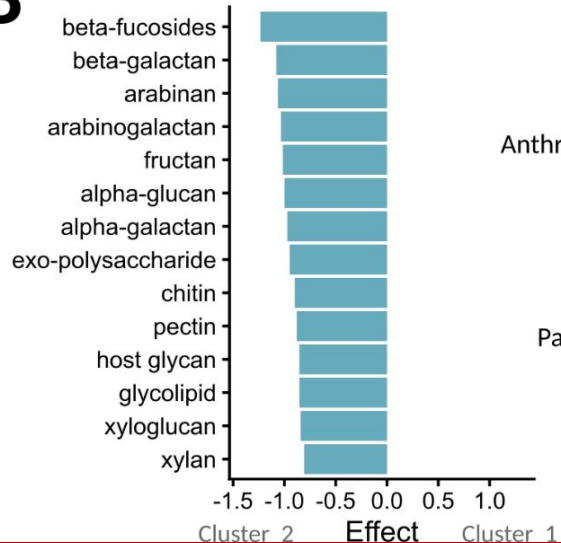


Seasonal differences explained by CAZYmes

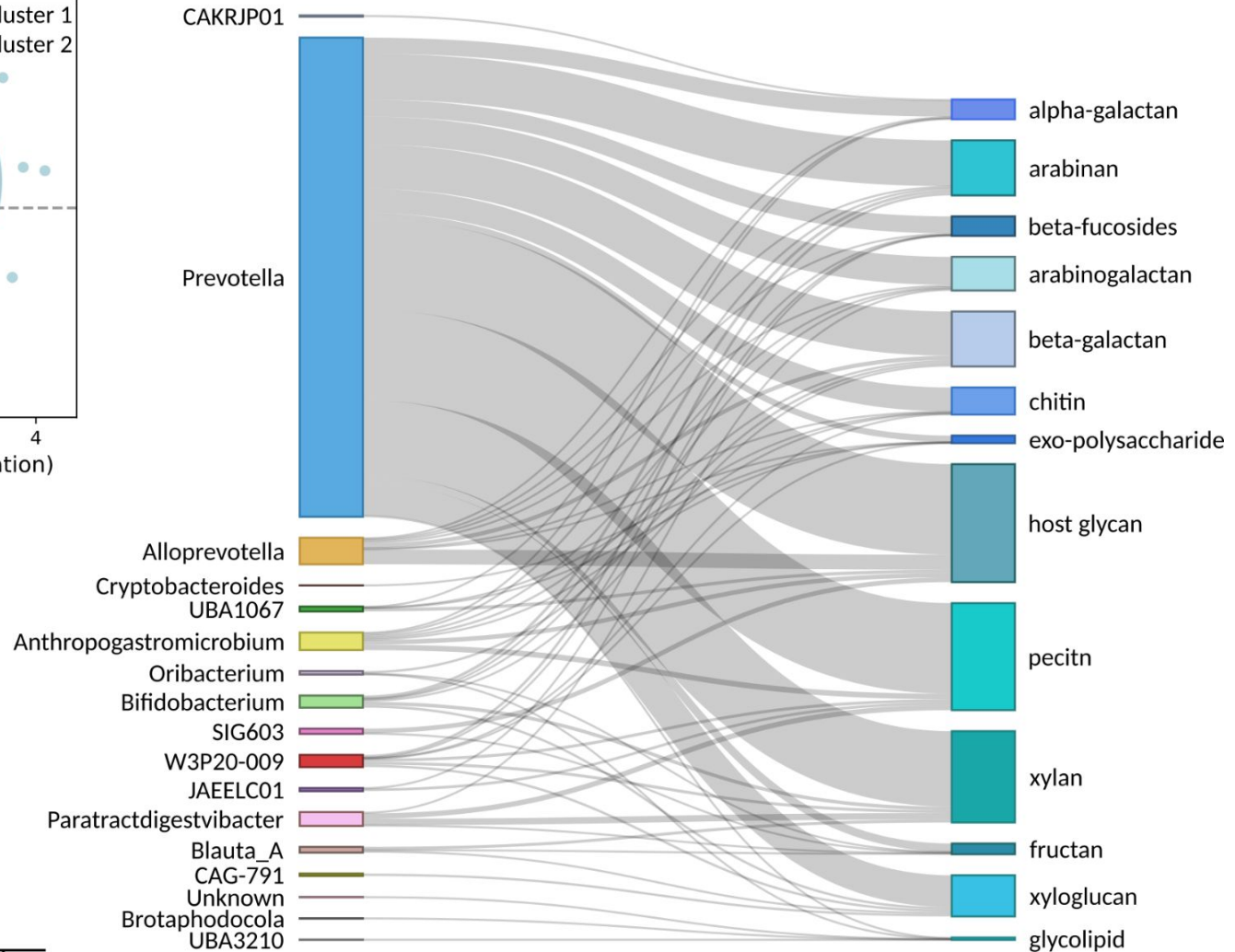
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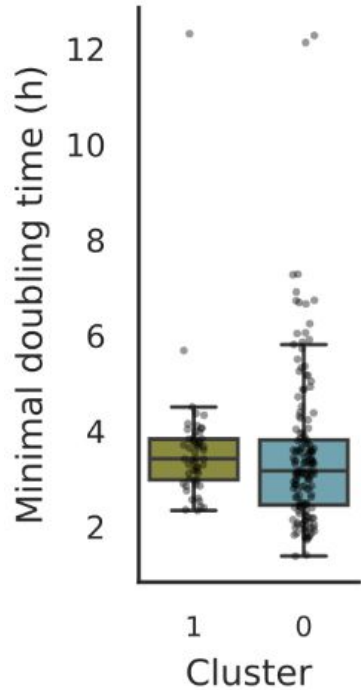


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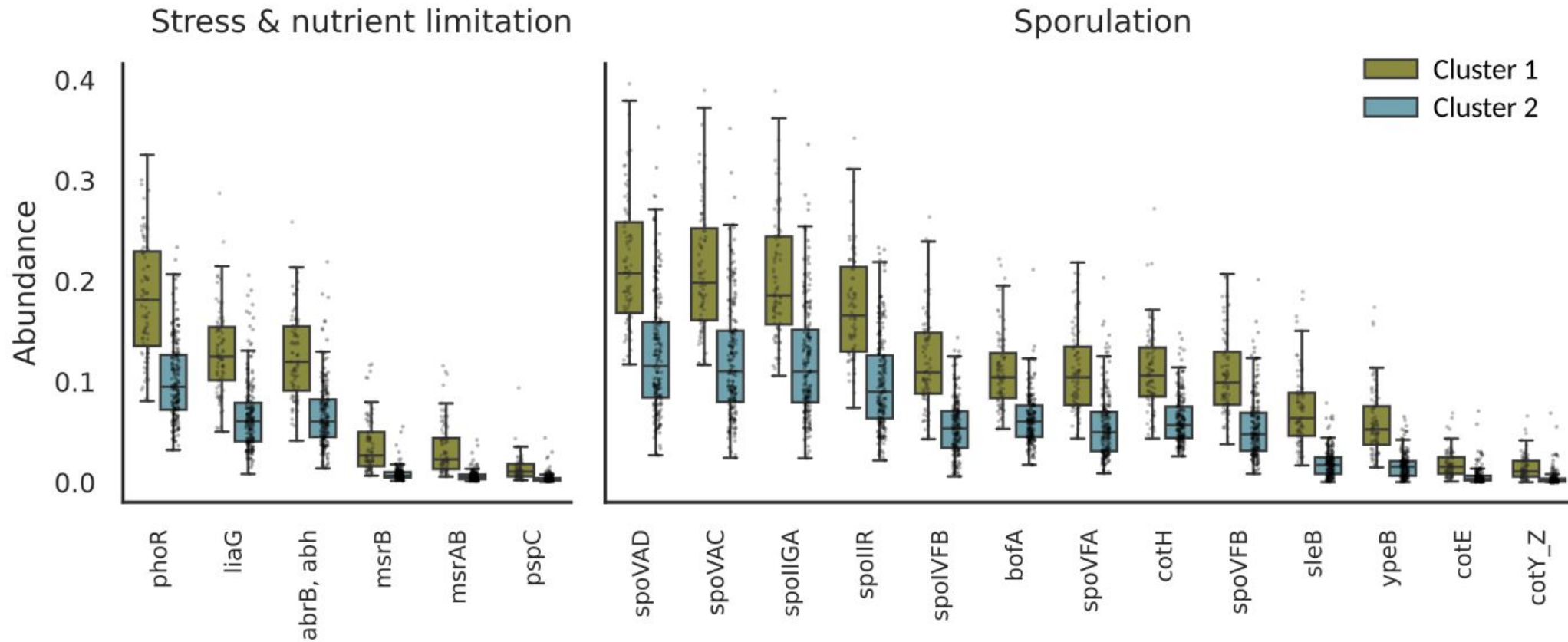


Seasonal differences explained by stress tolerance

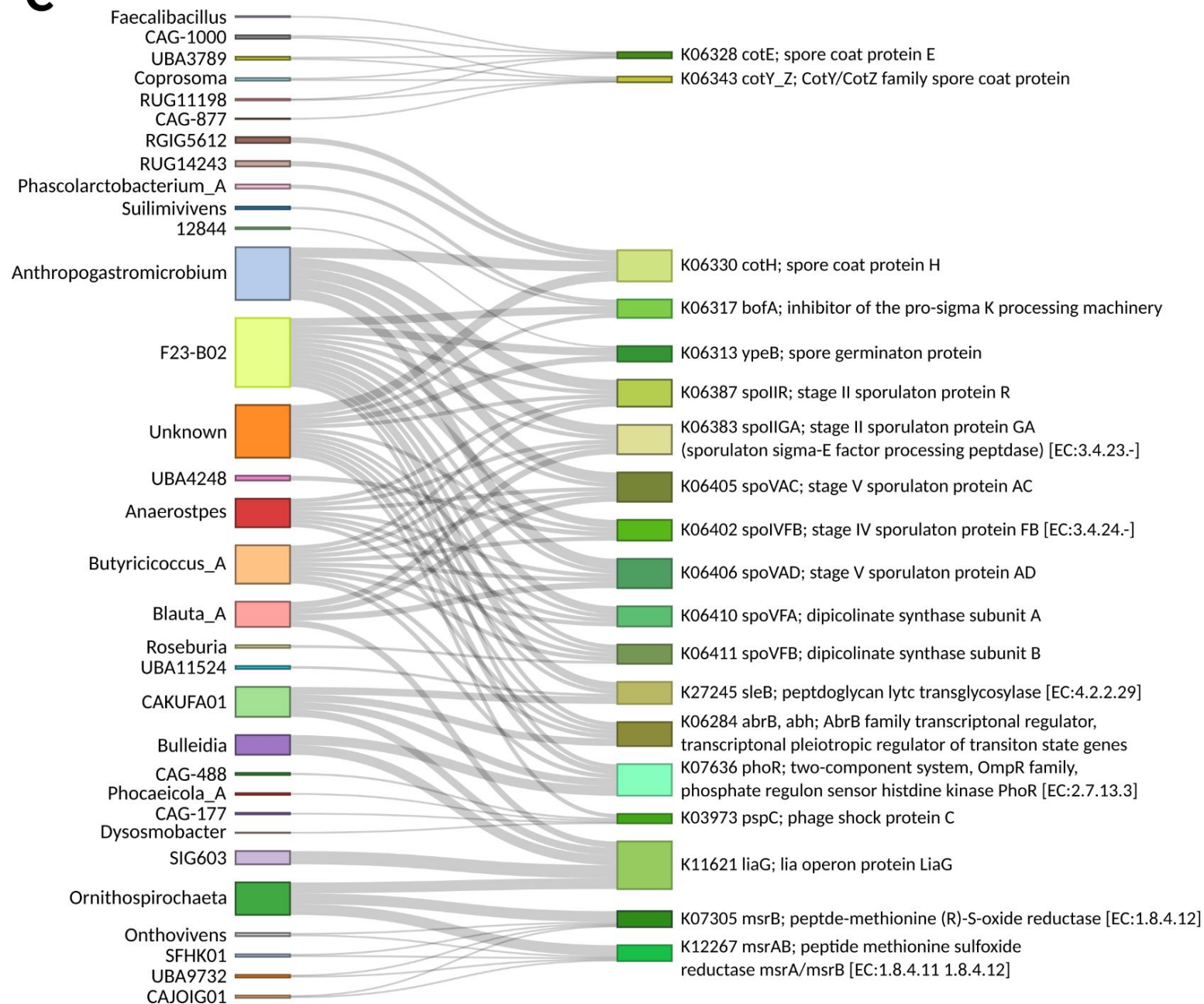
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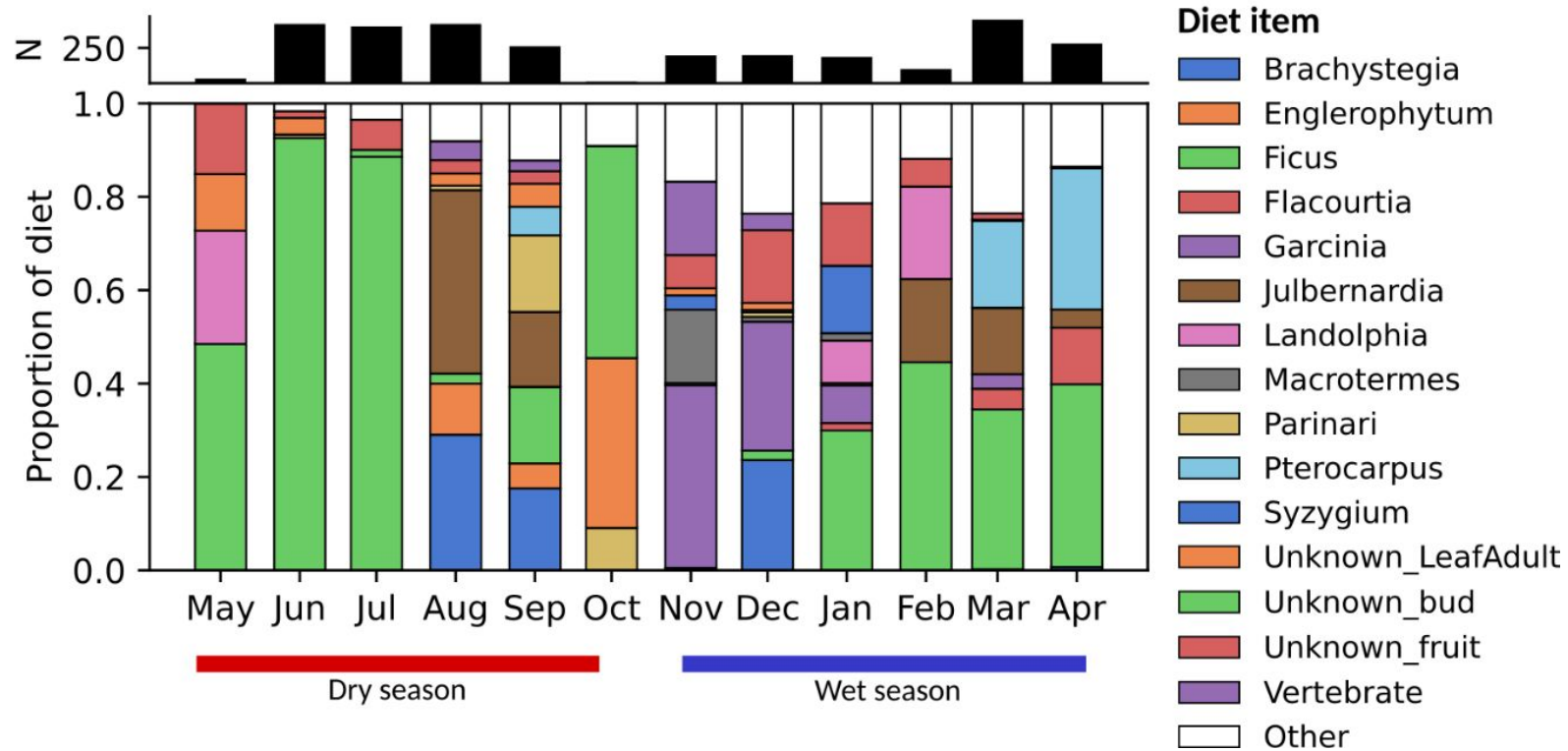
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C



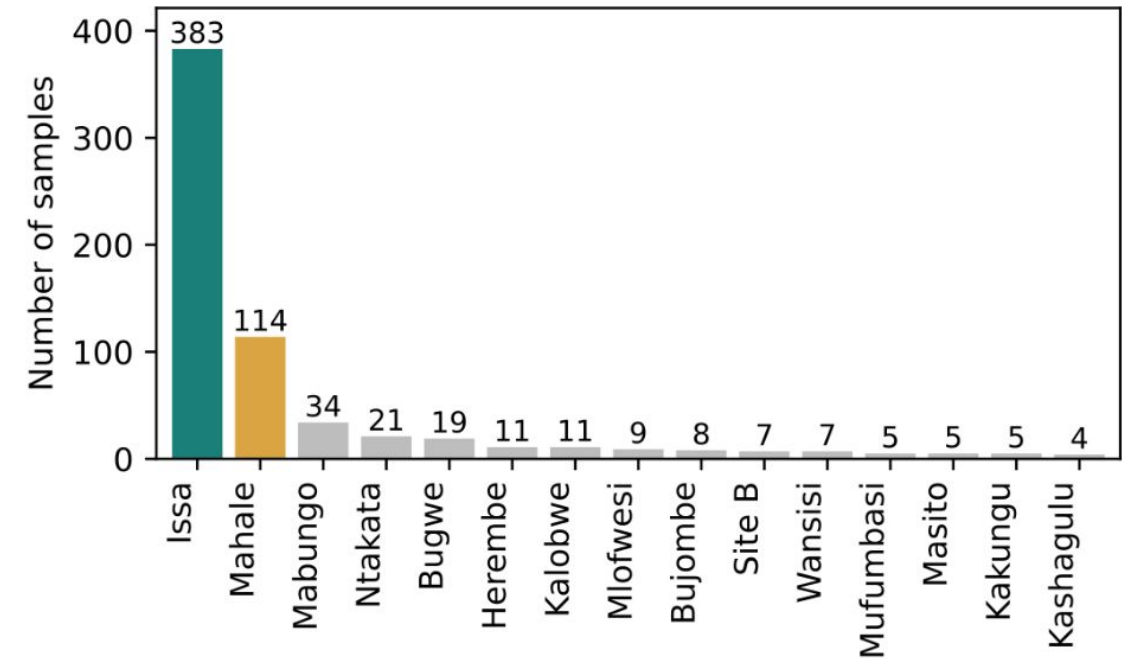
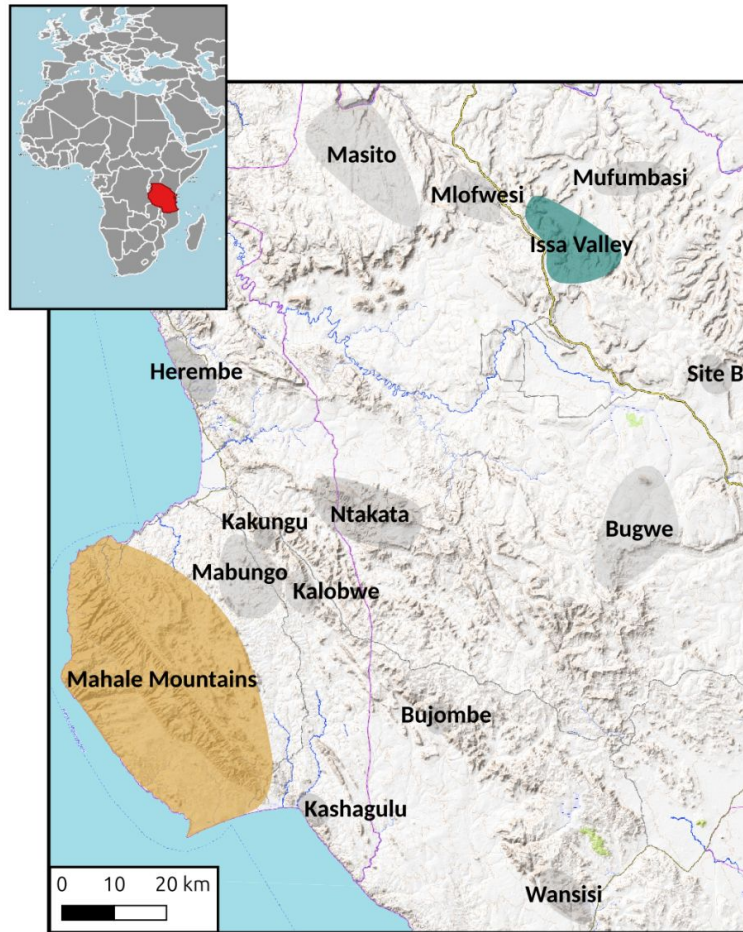
Fluctuating dietary resources shapes the gut microbiome of wild Tanzanian chimpanzees



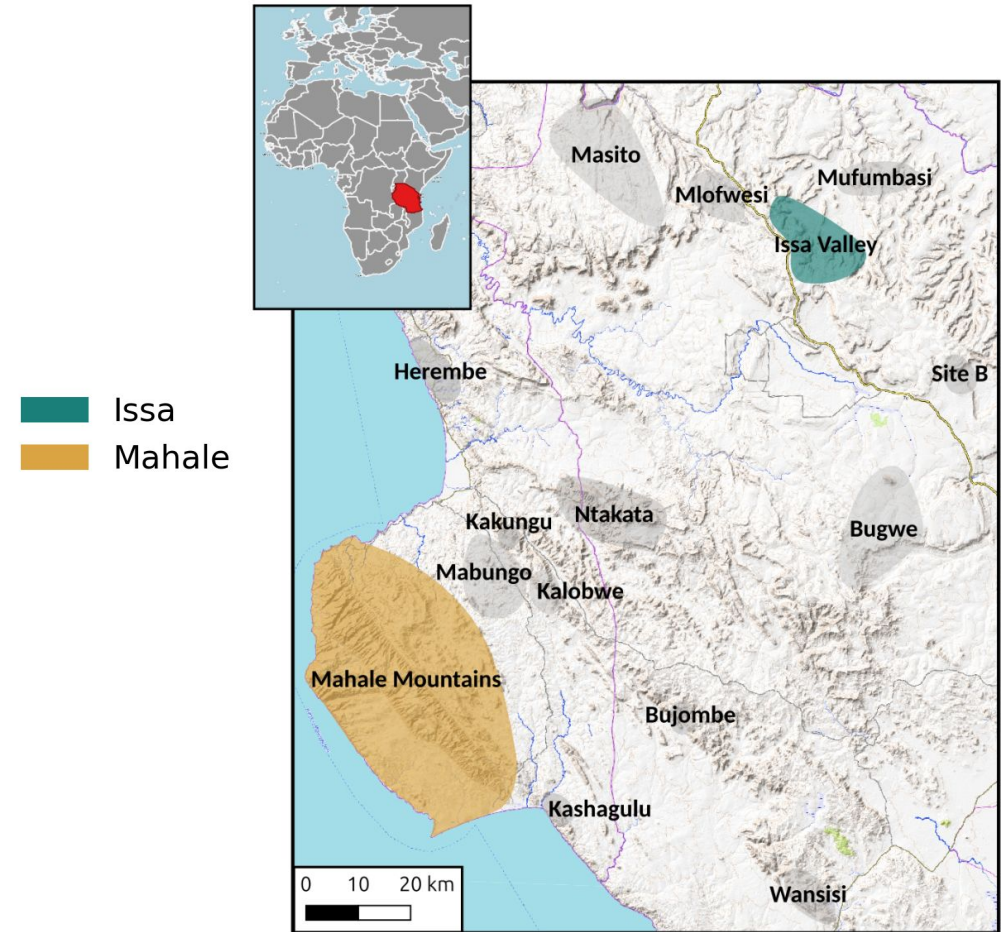
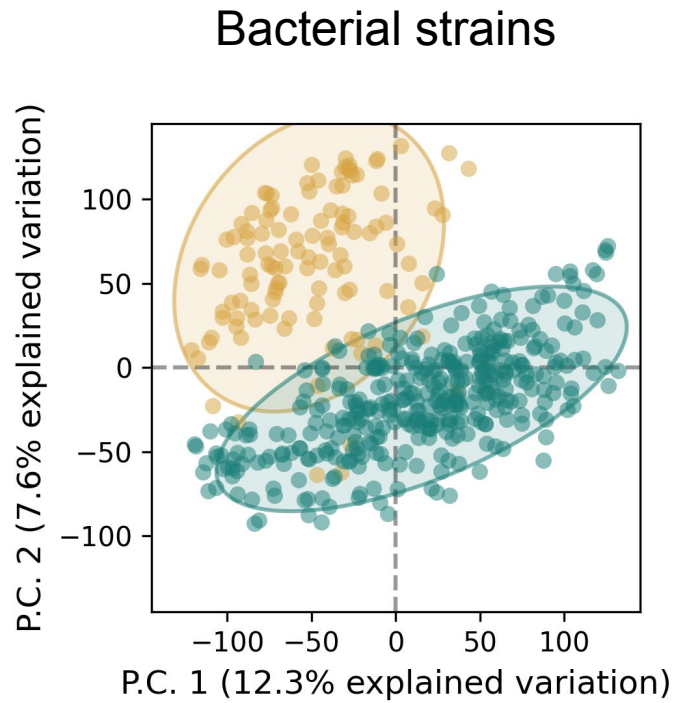
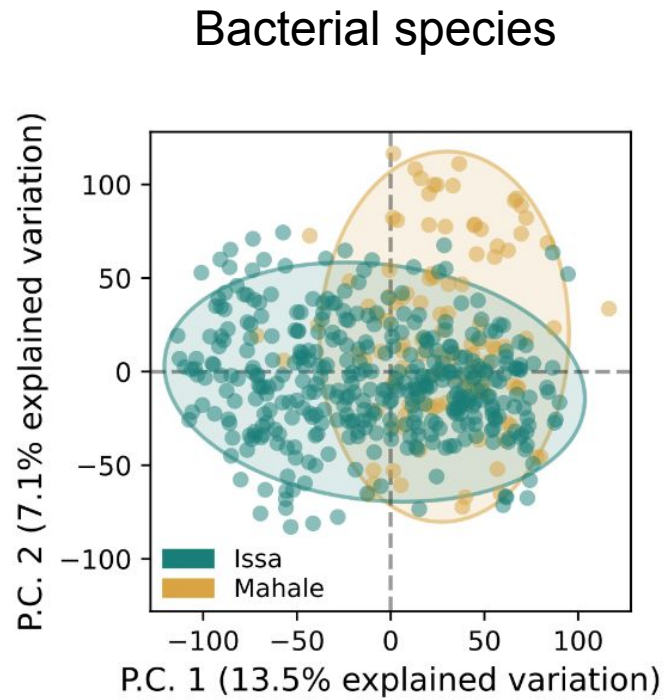
How does this expand on existing literature?

- Seasonality has been linked to changes in the gut microbiome composition (16S rRNA seq, Hicks et al. 2018)
 - 16 faecal samples from *P.t. troglodytes* (8 dry season, 8 wet season)
- Spatial distribution and host genetics shape gut microbiome composition of wild African chimpanzees (16S rRNA seq, De Mesquita et al. 2021)
 - 560 chimp faecal samples; 134 from *P.t. schweinfurthii*
- First shotgun metagenomic sequencing of wild chimpanzee gut microbiomes in 2024 (Rühleman et al. 2024)
 - 96 chimp faecal samples; 12 samples from *P.t. schweinfurthii*

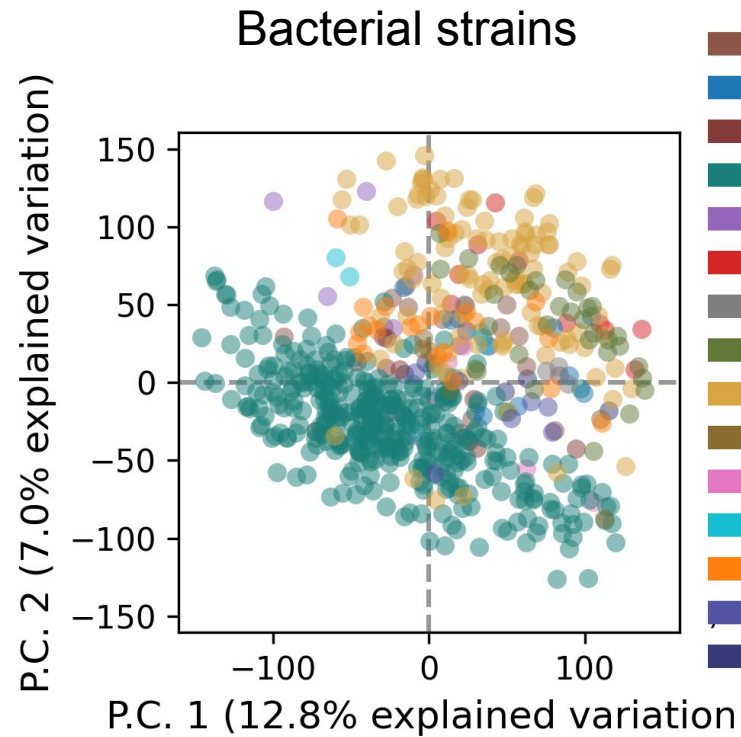
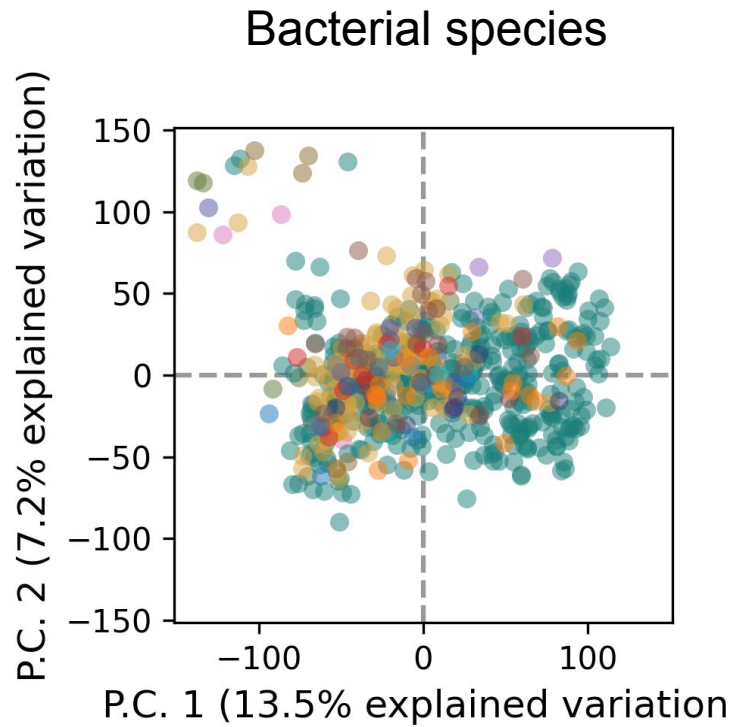
Does location impact the gut microbiome composition?



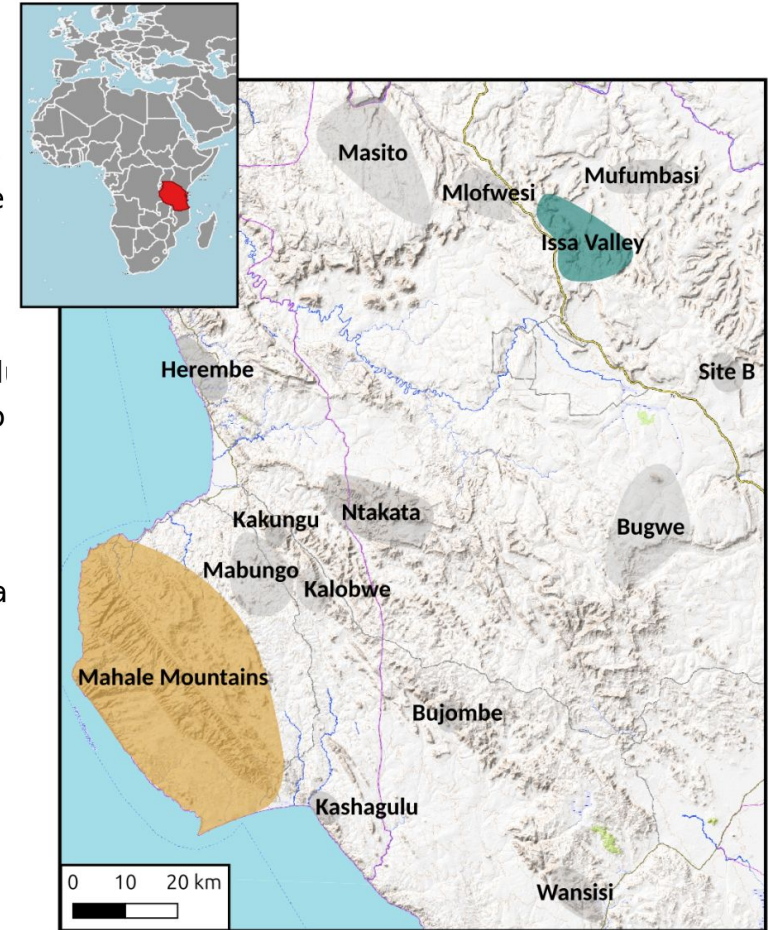
Does location impact the gut microbiome composition?



Does location impact the gut microbiome composition?

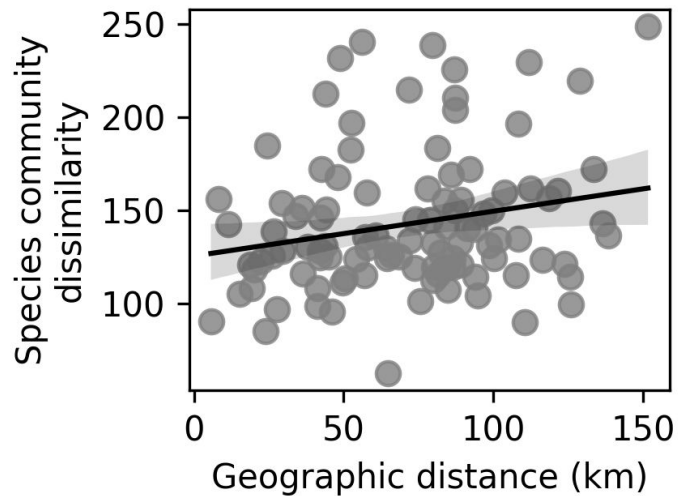


- Bugwe
- Bujombe
- Herembe
- Issa
- Kakungu
- Kalobwe
- Kashagulu
- Mabungo
- Mahale
- Masito
- Mlofwesi
- Mufumba
- Ntakata
- Site B
- Wansisi



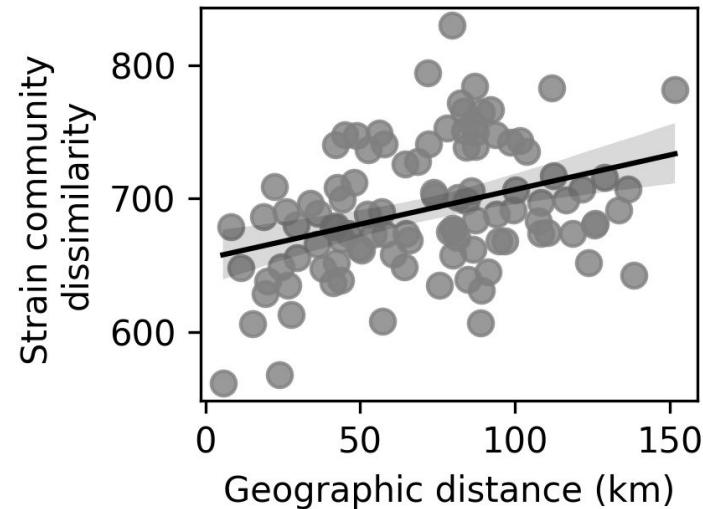
Does location impact the gut microbiome composition?

Bacterial species

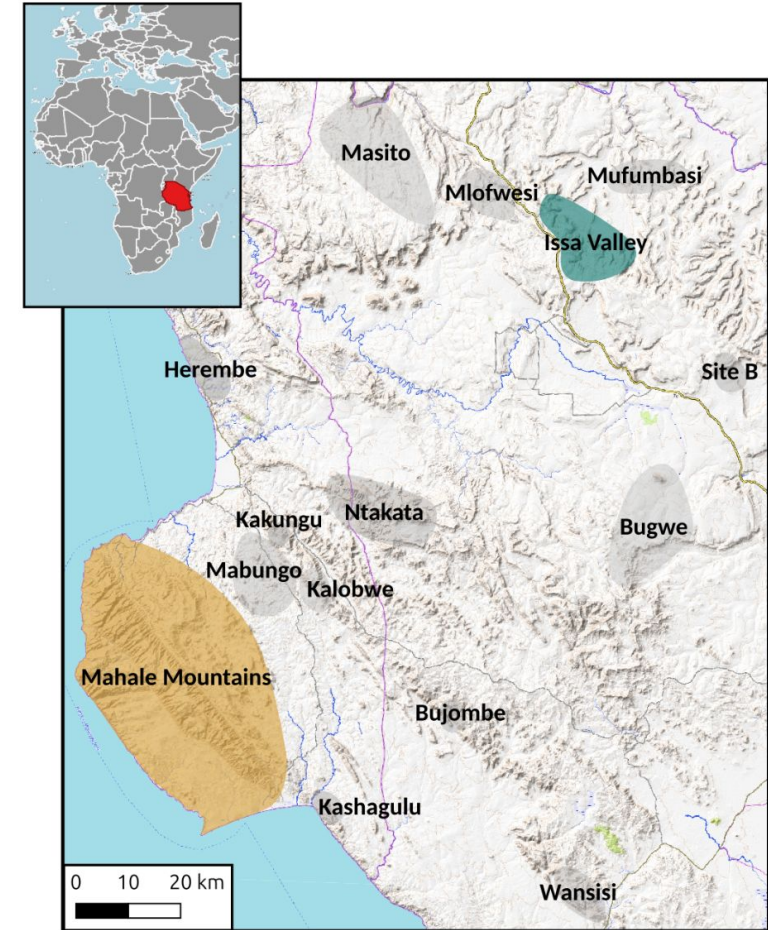


Mantel $r = 0.193$,
Mantel $p = 0.13690$

Bacterial strains

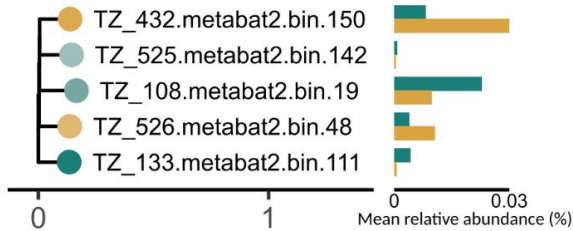


Mantel $r = 0.339$,
Mantel $p = 0.0033$

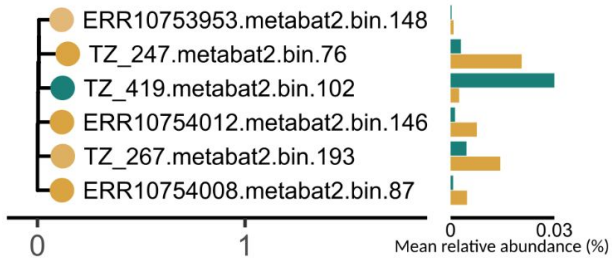


Does location impact the gut microbiome composition?

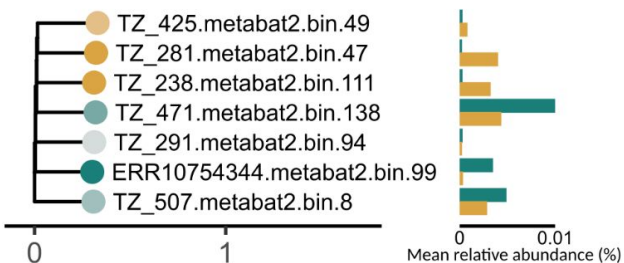
Sarcina ventriculi



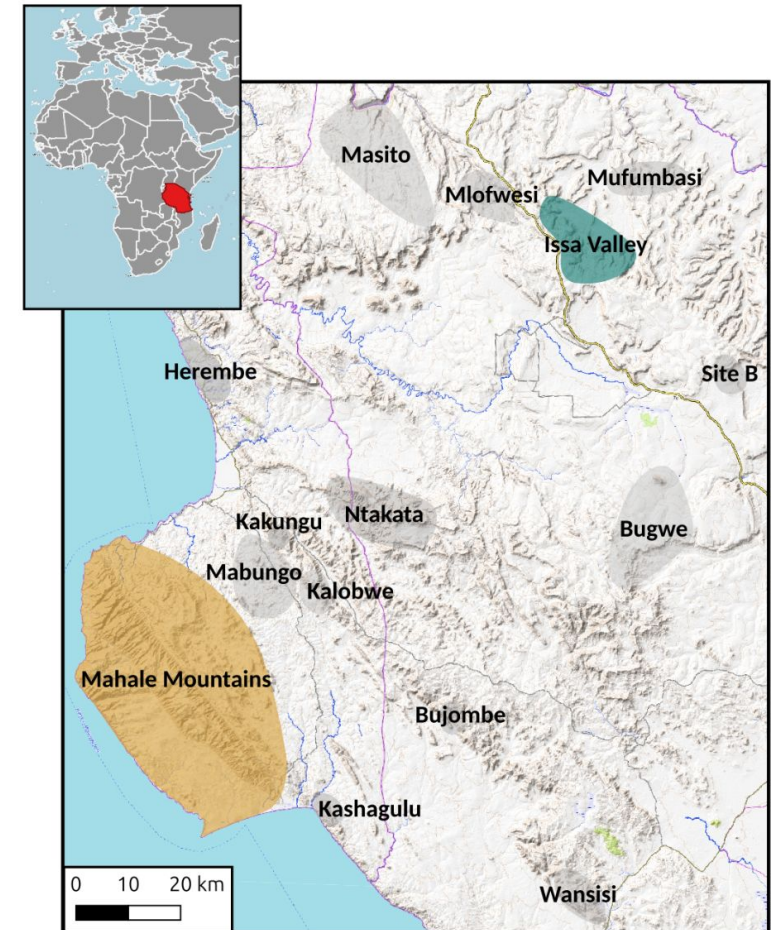
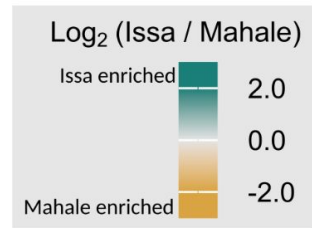
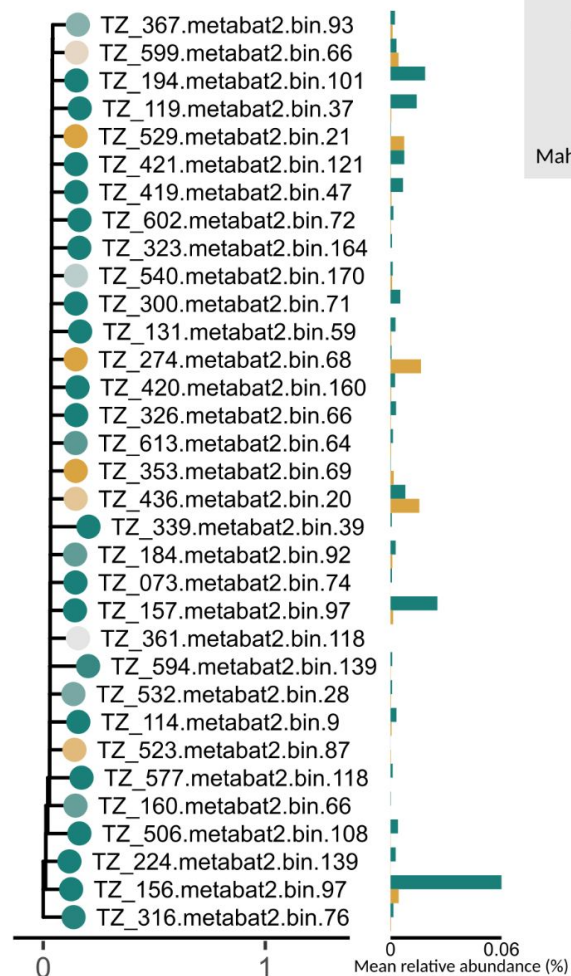
CAG-269 sp934167735



Aphodocola sp934141615



Roseburia sp934309475



Project #4

Genome reference project

Reference genome project

- TZ Goats: **6.92%** of trimmed reads aligned to bacterial reference database
- TZ chimps: **1.6%** of the trimmed reads aligned to NCBI bacterial reference database

Open Peer Review | Environmental Microbiology | Research Article

Tanzanian goat gut microbiomes adapt to roadside pollutants and environmental stressors

Emilie Egholm Bruun Jensen,¹ Marie Louise Jespersen,¹ Christina Aaby Svendsen,¹ Tolbert Sonda,² Saria Otani,¹ Frank M. Aarestrup¹

AUTHOR AFFILIATIONS See affiliation list on p. 14.

ABSTRACT The impact of environmental pollution reaching and affecting the gut microbiome is rising. Pollution from vehicle emissions can release compounds harmful to both animal and environmental health, and their effect on the host microbiome is yet to be determined, particularly in understudied locations. Here, we have investigated the potential effect of environmental pollution on the gut microbiome of Tanzanian goats grazing near a heavily trafficked road compared to goats living in a more rural setting. We identified 1,468 metagenome-assembled genomes (MAGs), of which 768 were unidentified species, and created a genomic database to which 52% of the bacterial community could be assigned. We find significant differences in the composition of the bacterial communities and resistomes between rural and road-exposed goats, but

Prior to the addition of the MAGs to the genomic database, only 6.92% of the trimmed reads aligned. However, on average, 51.83% of the trimmed reads aligned per sample to the custom genomic database consisting of the dereplicated MAGs, closed bacterial genomes, and draft genomes from NCBI Genbank. A total of 51.47% of the aligned reads were annotated as belonging to any taxonomic level of the superkingdom Bacteria. The aligned per-sample fragment counts to each of the databases and the percent of reads aligned to the databases are shown in Fig. S1 and Table S1, respectively.

Reference genome project

- TZ Goats: **6.92%** of trimmed reads aligned to bacterial reference database
- TZ chimps: **1.6%** of the trimmed reads aligned to NCBI bacterial reference database

Can we improve this?

Open Peer Review | Environmental Microbiology | Research Article

Tanzanian goat gut microbiomes adapt to roadside pollutants and environmental stressors

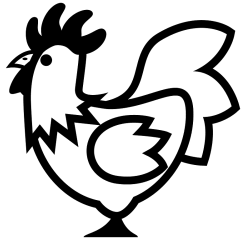
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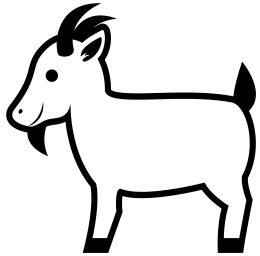
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Reference genome project



x4



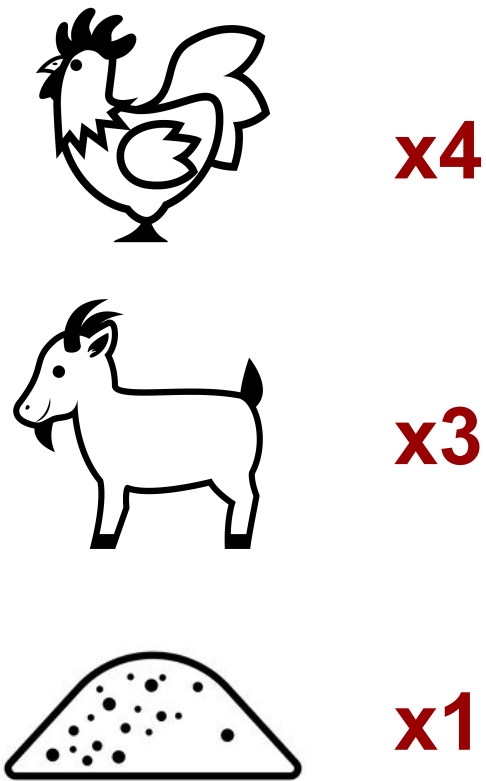
x3



x1



Reference genome project



Anaerobic + aerobic culturing



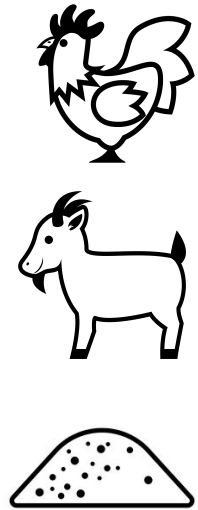
WGS



Assembly and classification



Reference genome project



Source	Oxygen	Total	Circular assemblies
Chicken	Aerobic	16	12
Chicken	Anaerobic	13	4
Goat	Aerobic	16	8
Goat	Anaerobic	13	9
Soil	Aerobic	4	2
Soil	Anaerobic	4	4
Total	Aerobic	36	22
Total	Anaerobic	30	17
Grand total		66	39

Reference genome project

Aerobic				
Species	Chicken	Goat	Soil	Total
<i>Escherichia coli</i>	4	1	1	6
<i>Enterococcus faecalis</i>	2			2
<i>Micrococcus luteus</i>	2		1	3
<i>Paenibacillus silvae</i>		1		1
<i>Paenibacillus_B alvei_B</i>		1		1
<i>Enterococcus_D casseliflavus</i>		2		2
<i>Prescottella equi</i>		2		2
<i>Bacillus altitudinis</i>		1		1
<i>Paenibacillus polysaccharolyticus</i>		1		1
<i>Enterobacter hormaechei_B</i>		1		1

Anaerobic				
Species	Chicken	Goat	Soil	Total
<i>Escherichia coli</i>	3	1		4
<i>Enterococcus_E cecorum</i>	1			1
<i>Enterococcus faecalis</i>		2		2
<i>Enterococcus_D casseliflavus</i>		1		1
<i>Enterococcus_B mundtii_C</i>		2		2
<i>Streptococcus equinus</i>		1		1
<i>Prescottella equi</i>		1		1
<i>Klebsiella variicola</i>		1		1
<i>Propionibacterium sp.</i>		1		1
<i>Sinomonas spp.</i>			1	1
<i>Staphylococcus warneri</i>			1	1
<i>Intrasporangium_A sp035707905</i>			1	1
<i>Microvirga sp.</i>			1	1

Reference genome project

Aerobic				
Species	Chicken	Goat	Soil	Total
<i>Escherichia coli</i>	4	1		5
<i>Enterococcus faecalis</i>	2			2
<i>Micrococcus luteus</i>	2			2
<i>Paenibacillus silvae</i>				1
<i>Paenibacillus_B alvei_B</i>		1		1
<i>Enterococcus_D casseliflavus</i>		2		2
<i>Prescottella equi</i>		2		2
<i>Bacillus altitudinis</i>		1		1
<i>Paenibacillus polysaccharolyticus</i>		1		1
<i>Enterobacter hormaechei_B</i>		1		1

... and chimps!

Anaerobic				
Species	Chicken	Goat	Soil	Total
<i>Escherichia coli</i>	3	1		4
<i>Enterococcus_E</i>	1			1
<i>Enterococcus faecalis</i>		2		2
<i>Enterococcus_D</i>		1		1
<i>Enterococcus_B mundtii_C</i>		2		2
<i>Streptococcus equinus</i>		1		1
<i>Prescottella equi</i>		1		1
<i>Klebsiella variicola</i>		1		1
<i>Propionibacterium sp.</i>		1		1
<i>Sinomonas spp.</i>			1	1
<i>Staphylococcus warneri</i>			1	1
<i>Intrasporangium_A sp035707905</i>			1	1
<i>Microvirga sp.</i>			1	1

Questions?

